

SEQUENCE LISTING.txt
SEQUENCE LISTING

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<120> Mutant Bacillus

<130> KS0816

<150> JP 2004-062852

<151> 2004.03.05

<160> 28

<170> PatentIn Ver. 3.1

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<211> 371

<212> PRT

<213> Bacillus subtilis

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Met Asp Glu Tyr Tyr Glu Phe Leu Gly Glu Gln Gly Val Glu Leu Ile
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Ser Glu Asn Glu Glu Thr Glu Asp Pro Asn Ile Gln Gln Leu Ala Lys
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Ala Glu Glu Glu Phe Asp Leu Asn Asp Leu Ser Val Pro Pro Gly Val
85 90 95

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 Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile
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 Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
 165 170 175
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 195 200 205
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 210 215 220
 Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala

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775

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Met Met Leu Arg Lys Lys Thr
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Gln	Lys	Glu	Ala	Glu	Lys	Glu	Glu	Lys	Glu	Ala	Val	Lys	Glu	Glu	Lys																
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SEQUENCE LISTING.txt

Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu
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50 55 60

Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
65 70 75 80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
85 90 95

Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
100 105 110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
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Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145 150 155 160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
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Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
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Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
195 200 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
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Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225 230 235 240

Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
245 250 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
260 265 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
275 280 285

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Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
325 330 335

Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
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Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
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Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
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Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
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Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
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Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp
420 425 430

Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
435 440 445

Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro
450 455 460

Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val
465 470 475 480

Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu
485 490 495

Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His
500 505 510

Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu
515 520 525

Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu
530 535 540

Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
545 550 555 560

SEQUENCE LISTING.txt

Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
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Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
595 600 605

Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg
610 615 620

Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg
625 630 635 640

Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr
645 650 655

Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp
660 665 670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val
675 680 685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
690 695 700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
705 710 715 720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
725 730 735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
740 745 750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
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cctgatttta tttttttgaa tttttttgag aactaaagat tgaaatagaa gtagaagaca 180

acggacataa gaaaattgta ttagttttta ttatagaaaa cgcttttcta taattattta 240

tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc 300

tttttttaaa caggggggtga aaattcactc tagtattcta atttcaacat gctataataa 360

atttgtaaga cgcaatatac atcttttttt tatgatattt gtaagcgggtt aaccttgtgc 420

tatatgccga tttaggaagg gggtagattg agtcaagtag tcataattta gataacttat 480

aagttgttga gaagcaggag agaatctggg ttactcacia gttttttaaa acattatcga 540

aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta 600

ggaggtaat atg atg tta aga aag aaa aca aag cag ttg att tct tcc att 651
Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile
-25 -20

ctt att tta gtt tta ctt cta tct tta ttt ccg aca gct ctt gca gca 699
Leu Ile Leu Val Leu Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala
-15 -10 -5 -1 1

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5 10 15

aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc 795
Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val
20 25 30

gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa tta 843
Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu
35 40 45

cgt gga atg agt aca cac gga tta caa tgg ttt cct gag atc ttg aat 891
Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn
50 55 60 65

gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg att 939
Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile
70 75 80

cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca gag 987
Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu
85 90 95

tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa aat 1035
Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn
100 105 110

SEQUENCE LISTING.txt

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aga Arg 130	gat Asp	ccc Pro	gtt Val	tac Tyr	gct Ala 135	gga Gly	gca Ala	gaa Glu	gat Asp	ttc Phe 140	ttt Phe	aga Arg	gat Asp	att Ile	gca Ala 145	1131
gca Ala	tta Leu	tat Tyr	cct Pro	aac Asn 150	aat Asn	cca Pro	cac His	att Ile	att Ile 155	tat Tyr	gag Glu	tta Leu	gcg Ala	aat Asn 160	gag Glu	1179
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aac Asn 210	tgg Trp	agt Ser	cag Gln	cgt Arg	cct Pro 215	gac Asp	tta Leu	gca Ala	gct Ala	gat Asp 220	aat Asn	cca Pro	att Ile	gat Asp	gat Asp 225	1371
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tat Tyr	gta Val 355	cgt Arg	gct Ala	cgt Arg	att Ile	aaa Lys 360	ggt Gly	gtg Val	aac Asn	tat Tyr	gag Glu 365	cca Pro	atc Ile	gac Asp	cgt Arg	1803
aca Thr 370	aaa Lys	tac Tyr	acg Thr	aaa Lys	gta Val 375	ctt Leu	tgg Trp	gac Asp	ttt Phe	aat Asn 380	gat Asp	gga Gly	acg Thr	aag Lys	caa Gln 385	1851

SEQUENCE LISTING.txt

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gtt tct gaa ggt aat tac tgg gct aat gct cgt ctt tct gcc gac ggt Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly 420 425 430	1995
tgg gga aaa agt gtt gat att tta ggt gct gaa aaa ctt act atg gat Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp 435 440 445	2043
gtg att gtt gat gag ccg acc acg gta tca att gct gca att cca caa Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln 450 455 460 465	2091
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cca act aat ttc gta ccg tta gga gat aag ttt aaa gcg gaa tta act Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr 485 490 495	2187
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aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn 645 650 655	2667

SEQUENCE LISTING.txt

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665	
670	
tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa	2763
Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys	
675	
680	
685	
att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt	2811
Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg	
690	
695	
700	
705	
aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga	2859
Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg	
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715	
720	
gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg	2907
Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro	
725	
730	
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gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat	2955
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745	
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gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa	3003
Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys	
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gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca	3051
Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala	
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775	
780	
785	
atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct	3105
Ile Lys Asn Glu Ala Thr Lys Lys	
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aaaggctctga tgcagatctt ttagataacc tttttttgca taactggaca tagaatgggtt	3165
attaaagaaa gcaagggtgtt tatacgatat taaaaaggta gcgatttttaa attgaaacct	3225
ttaataatgt cttgtgatag aatgatgaag taatttaaga gggggaaaacg aagtgaaaac	3285
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<220>
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<210> 9
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 <212> DNA
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<220>
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SEQUENCE LISTING.txt

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SEQUENCE LISTING.txt

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<210> 17
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<212> DNA
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<220>
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aaatgacatc atataaaciaa atttgtctac caatcactat ttaaagctgt ttatgatata	180
tgtaagcggt atcattaaaaa ggagggtatgt g atg aga aga tgg gta gta gca	232
Met Arg Arg Trp Val Val Ala	-20 -15
atg ttg gca gtg tta ttt tta ttt cct tct gta gta gtt gca gat gga	280
Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala Asp Gly	-10 -5 -1 1
ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa aac gac	328
Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp	5 10 15
ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat	376
Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Leu Ser Asp	20 25 30
gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt aat agt	424
Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser	35 40 45 50
cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag	472
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	55 60 65
ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag gca cag	520
Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln	70 75 80
ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat gta tac	568
Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr	85 90 95
gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg gag gca	616
Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala	100 105 110
gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat att tca	664
Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp Ile Ser	115 120 125 130
ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt	712
Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg	135 140 145
aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt	760
Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly	150 155 160
gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca	808
Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala	165 170 175
aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat	856
Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp	180 185 190
tac ctg tta gga tct aat atc gac ttt agt cat cca gaa gta caa gat	904
Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp	195 200 205 210

SEQUENCE LISTING.txt

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ggt	tat	cgt	tta	gat	gct	att	aaa	cat	att	cca	ttc	tgg	tat	aca	tct	1000
Gly	Tyr	Arg	Leu	Asp	Ala	Ile	Lys	His	Ile	Pro	Phe	Trp	Tyr	Thr	Ser	
			230					235					240			
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Asp	Trp	Val	Arg	His	Gln	Arg	Asn	Glu	Ala	Asp	Gln	Asp	Leu	Phe	Val	
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Val	Gly	Glu	Tyr	Trp	Lys	Asp	Asp	Val	Gly	Ala	Leu	Glu	Phe	Tyr	Leu	
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gat	gaa	atg	aat	tgg	gag	atg	tct	cta	ttc	gat	ggt	cca	ctt	aat	tat	1144
Asp	Glu	Met	Asn	Trp	Glu	Met	Ser	Leu	Phe	Asp	Val	Pro	Leu	Asn	Tyr	
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aat	ttt	tac	cgg	gct	tca	caa	caa	ggt	gga	agc	tat	gat	atg	cgt	aat	1192
Asn	Phe	Tyr	Arg	Ala	Ser	Gln	Gln	Gly	Gly	Ser	Tyr	Asp	Met	Arg	Asn	
				295					300					305		
att	tta	cga	gga	tct	tta	gta	gaa	gcg	cat	ccg	atg	cat	gca	gtt	acg	1240
Ile	Leu	Arg	Gly	Ser	Leu	Val	Glu	Ala	His	Pro	Met	His	Ala	Val	Thr	
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Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Glu	Ser	Leu	Glu	Ser	Trp	
		325					330					335				
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Val	Ala	Asp	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Thr	Ile	Leu	Thr	Arg	
	340					345				350						
gaa	ggt	ggt	tat	cca	aat	gta	ttt	tac	ggt	gat	tac	tat	ggg	att	cct	1384
Glu	Gly	Gly	Tyr	Pro	Asn	Val	Phe	Tyr	Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	
	355				360					365					370	
aac	gat	aac	att	tca	gct	aaa	aaa	gat	atg	att	gat	gag	ctg	ctt	gat	1432
Asn	Asp	Asn	Ile	Ser	Ala	Lys	Lys	Asp	Met	Ile	Asp	Glu	Leu	Leu	Asp	
				375					380					385		
gca	cgt	caa	aat	tac	gca	tat	ggc	acg	cag	cat	gac	tat	ttt	gat	cat	1480
Ala	Arg	Gln	Asn	Tyr	Ala	Tyr	Gly	Thr	Gln	His	Asp	Tyr	Phe	Asp	His	
			390					395					400			
tgg	gat	ggt	gta	gga	tgg	act	agg	gaa	gga	tct	tcc	tcc	aga	cct	aat	1528
Trp	Asp	Val	Val	Gly	Trp	Thr	Arg	Glu	Gly	Ser	Ser	Ser	Arg	Pro	Asn	
		405					410					415				
tca	ggc	ctt	gcg	act	att	atg	tcg	aat	gga	cct	ggt	ggt	tcc	aag	tgg	1576
Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asn	Gly	Pro	Gly	Gly	Ser	Lys	Trp	
	420					425					430					
atg	tat	gta	gga	cgt	cag	aat	gca	gga	caa	aca	tgg	aca	gat	tta	act	1624
Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Gln	Thr	Trp	Thr	Asp	Leu	Thr	
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ggt	aat	aac	gga	gcg	tcc	gtt	aca	att	aat	ggc	gat	gga	tgg	ggc	gaa	1672
Gly	Asn	Asn	Gly	Ala	Ser	Val	Thr	Ile	Asn	Gly	Asp	Gly	Trp	Gly	Glu	
				455					460					465		
ttc	ttt	acg	aat	gga	gga	tct	gta	tcc	gtg	tac	gtg	aac	caa	taacaaaaa	1723	
Phe	Phe	Thr	Asn	Gly	Gly	Ser	Val	Ser	Val	Tyr	Val	Asn	Gln			
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tctacgactt tg 1795

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20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220

SEQUENCE LISTING.txt

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
 225 230 235 240
 Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
 245 250 255
 Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
 260 265 270
 Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
 275 280 285
 Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
 290 295 300
 Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
 325 330 335
 Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
 340 345 350
 Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
 355 360 365
 Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
 370 375 380
 Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
 385 390 395 400
 Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
 405 410 415
 Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
 420 425 430
 Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
 435 440 445
 Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
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 Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
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<213> Bacillus clausii KSM-K16

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taccagcttg gacgagttgg gataaaagtg aggagggaac cga atg aag aaa ccg	175
	Met Lys Lys Pro
	1
ttg ggg aaa att gtc gca agc acc gca cta ctc att tct gtt gct ttt	223
Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile Ser Val Ala Phe	20
5	10
agt tca tcg atc gca tcg gct gct gag gaa gca aaa gaa aaa tat tta	271
Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys Glu Lys Tyr Leu	35
25	30
att ggc ttt aat gag cag gaa gca gtt agt gag ttt gta gag caa ata	319
Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe Val Glu Gln Ile	40
40	45
gag gca aat gac gat gtc gcg att ctc tct gag gaa gag gaa gtc gaa	367
Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu Glu Glu Val Glu	55
55	60
att gaa ttg ctt cat gag ttt gaa acg att cct gtt tta tct gtt gag	415
Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val Leu Ser Val Glu	70
70	75
tta agt cca gaa gat gtg gac gcg ctt gag ctc gat cca acg att tcg	463
Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp Pro Thr Ile Ser	90
85	95
tat att gaa gag gat gca gaa gta acg aca atg gcg caa tca gtg cca	511
Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala Gln Ser Val Pro	105
105	110
tggt gga att agc cgt gta caa gcc cca gct gcc cat aac cgt gga ttg	559
Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His Asn Arg Gly Leu	120
120	125
aca ggt tct ggt gta aaa gtt gct gtc ctc gat acg ggt att tcc acc	607
Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr Gly Ile Ser Thr	135
135	140
cat cca gac tta aat att cgc ggt ggt gct agc ttt gtg cca gga gaa	655
His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe Val Pro Gly Glu	150
150	155
cca tcc act caa gat gga aat gga cat ggc acg cat gtg gca ggg acg	703
Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His Val Ala Gly Thr	165
165	170
att gct gct tta aac aat tcg att ggc gtt ctg ggc gta gca ccg agc	751
Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser	185
185	190
gcg gaa cta tac gct gta aaa gta tta ggc gcg agc ggt tca ggt tcg	799
Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser Gly Ser Gly Ser	200
200	205
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SEQUENCE LISTING.txt

gtc agc tcg att gcc caa gga ttg gaa tgg gca ggg aac aat ggc atg	847
Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly Asn Asn Gly Met	
215	
cac gtt gcg aat ttg agt tta gga agc ccg tcg ccg agt gca aca ctt	895
His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro Ser Ala Thr Leu	
230	
235	
240	
gag caa gct gtt aat agc gct act tct aga ggc gtt ctt gtc gta gca	943
Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val Leu Val Val Ala	
245	
250	
255	
260	
gca tct ggt aat tca ggt gca ggc tca atc agc tat ccg gcc cgt tat	991
Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr Pro Ala Arg Tyr	
265	
270	
275	
gcg aac gca atg gca gtc gga gcg act gac caa aac aac aac cgc gct	1039
Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn Asn Asn Arg Ala	
280	
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290	
agc ttt tca cag tat gga gct ggg ctt gac att gtc gcg cca ggt gtc	1087
Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val Ala Pro Gly Val	
295	
300	
305	
aat gtg cag agc aca tac cca ggt tca aca tat gcc agc tta aac ggt	1135
Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala Ser Leu Asn Gly	
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315	
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aca tcg atg gct act cct cat gtt gca ggt gta gca gcc ctt gtt aaa	1183
Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala Ala Leu Val Lys	
325	
330	
335	
340	
caa aag aat cca tct tgg tcc aat gta caa atc cgc aat cat cta aag	1231
Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg Asn His Leu Lys	
345	
350	
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aat acg gca acg ggt tta gga aac acg aac ttg tat gga agc ggg ctt	1279
Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr Gly Ser Gly Leu	
360	
365	
370	
gtc aat gca gaa gcg gca aca cgc taatcaataa taataacgct gtgtgcttta	1333
Val Asn Ala Glu Ala Ala Thr Arg	
375	
380	
agcacacagc gtttttttagt gtgtatgaat cgaaaaagag aaatagatcg ctgatttcaa	1393
aaagcgagcg taaagggcta ttgaagctct ttacgcttgc aggatttg	1441
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Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys	
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35 40 45	

SEQUENCE LISTING.txt

Val Glu Gln Ile Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu
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Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val
65 70 75 80

Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp
85 90 95

Pro Thr Ile Ser Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala
100 105 110

Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His
115 120 125

Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr
130 135 140

Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe
145 150 155 160

Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His
165 170 175

Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly
180 185 190

Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser
195 200 205

Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly
210 215 220

Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro
225 230 235 240

Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val
245 250 255

Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr
260 265 270

Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn
275 280 285

Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val
290 295 300

Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala
305 310 315 320

SEQUENCE LISTING.txt

Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala
325 330 335

Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg
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Asn His Leu Lys Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr
355 360 365

Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
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<210> 22
<211> 46
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline protease gene in *Bacillus clausii* KSM-K16 and its 5'-portion designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in *Bacillus* sp. KSM-S237

<400> 22
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<210> 23
<211> 32
<212> DNA
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<400> 23
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<210> 24
<211> 25
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide as PCR primer designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in *Bacillus* sp. KSM-S237 with a insertion of the BamHI restriction site at the 5'-end

<400> 24
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<210> 25
<211> 46
<212> DNA
<213> Artificial

SEQUENCE LISTING.txt

<220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in Bacillus sp. KSM-S237 and its 5'-portion designed from nucleotide sequence of the alkaline protease gene in Bacillus clausii KSM-K16

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<210> 26
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline amylase gene in Bacillus sp. KSM-K38 and its 5'-portion designed from nucleotide sequence of the alkaline cellulase gene in Bacillus sp. KSM-S237

<400> 26
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<210> 27
 <211> 30
 <212> DNA
 <213> Artificial

<220>
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<400> 27
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<210> 28
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline cellulase gene in Bacillus sp. KSM-S237 and its 5'-portion designed from nucleotide sequence of the alkaline amylase gene in Bacillus sp. KSM-K38

<400> 28
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